

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number:

09/155,514C

Source:

FFW/J6

Date Processed by STIC:

2-2-05

ENTERED



IFW16

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/155,514C

DATE: 02/02/2005

TIME: 16:44:04

Input Set : A:\1102-98.txt
 Output Set: N:\CRF4\02022005\I155514C.raw

```

4 <110> APPLICANT: Kainoh, Mie
5      Tanaka, Toshiaki
7 <120> TITLE OF INVENTION: Chimeric Proteins, their Heterodimer
8      Complexes, and Platelet Substitutes
12 <130> FILE REFERENCE: 1102-98
14 <140> CURRENT APPLICATION NUMBER: 09/155,514C
15 <141> CURRENT FILING DATE: 1998-11-17
17 <150> PRIOR APPLICATION NUMBER: WO PCT/JP98/00370
18 <151> PRIOR FILING DATE: 1998-01-29
20 <150> PRIOR APPLICATION NUMBER: JP 9-15118
21 <151> PRIOR FILING DATE: 1997-01-29
23 <150> PRIOR APPLICATION NUMBER: JP-9-234544
24 <151> PRIOR FILING DATE: 1997-08-29
26 <160> NUMBER OF SEQ ID NOS: 34
28 <170> SOFTWARE: FastSEQ for Windows Version 4.0
30 <210> SEQ ID NO: 1
31 <211> LENGTH: 4228
32 <212> TYPE: DNA
33 <213> ORGANISM: Artificial Sequence
35 <220> FEATURE:
36 <223> OTHER INFORMATION: sequence encoding fusion protein
W--> 38 <221> NAME/KEY: CDS
39 <222> LOCATION: (1)...(2958)
W--> 41 <221> CDS
42 <222> LOCATION: (3316)...(3360)
W--> 44 <221> CDS
45 <222> LOCATION: (3480)...(3808)
W--> 47 <221> CDS
48 <222> LOCATION: (3905)...(4228)
W--> 50 <400> 1
51 atg ttc ccc acc gag agc gca tgg ctt ggg aag cga ggc gcg aac ccg      48
52 Met Phe Pro Thr Glu Ser Ala Trp Leu Gly Lys Arg Gly Ala Asn Pro
53   1           5           10          15
55 ggc ccc gaa gct gca ctc cgg gag acg gtg atg ctg ttg ctg tgc ctg      96
56 Gly Pro Glu Ala Ala Leu Arg Glu Thr Val Met Leu Leu Leu Cys Leu
57   20          25           30
59 ggg gtc ccg acc ggc agg cct tac aac gtg gac act gag agc gcg ctg    144
60 Gly Val Pro Thr Gly Arg Pro Tyr Asn Val Asp Thr Glu Ser Ala Leu
61   35          40           45
63 ctt tac cag ggc ccc cac aac acg ctg ttc ggc tac tcg gtc gtg ctg    192
64 Leu Tyr Gln Gly Pro His Asn Thr Leu Phe Gly Tyr Ser Val Val Leu
65   50          55           60
67 cac agc cac ggg gcg aac cga tgg ctc cta gtg ggt gcg ccc act gcc    240

```

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68 His Ser His Gly Ala Asn Arg Trp Leu Leu Val Gly Ala Pro Thr Ala		
69 65 70 75 80		
71 aac tgg ctc gcc aac gct tca gtg atc aat ccc ggg gcg att tac aga	288	
72 Asn Trp Leu Ala Asn Ala Ser Val Ile Asn Pro Gly Ala Ile Tyr Arg		
73 85 90 95		
75 tgc agg atc gga aag aat ccc ggc cag acg tgc gaa cag ctc cag ctg	336	
76 Cys Arg Ile Gly Lys Asn Pro Gly Gln Thr Cys Glu Gln Leu Gln Leu		
77 100 105 110		
79 ggt agc cct aat gga gaa cct tgt gga aag act tgt ttg gaa gag aga	384	
80 Gly Ser Pro Asn Gly Glu Pro Cys Gly Lys Thr Cys Leu Glu Glu Arg		
81 115 120 125		
83 gac aat cag tgg ttg ggg gtc aca ctt tcc aga cag cca gga gaa aat	432	
84 Asp Asn Gln Trp Leu Gly Val Thr Leu Ser Arg Gln Pro Gly Glu Asn		
85 130 135 140		
87 gga tcc atc gtg act tgt ggg cat aga tgg aaa aat ata ttt tac ata	480	
88 Gly Ser Ile Val Thr Cys Gly His Arg Trp Lys Asn Ile Phe Tyr Ile		
89 145 150 155 160		
91 aag aat gaa aat aag ctc ccc act ggt ggt tgc tat gga gtg ccc cct	528	
92 Lys Asn Glu Asn Lys Leu Pro Thr Gly Gly Cys Tyr Gly Val Pro Pro		
93 165 170 175		
95 gat tta cga aca gaa ctg agt aaa aga ata gct ccg tgt tat caa gat	576	
96 Asp Leu Arg Thr Glu Leu Ser Lys Arg Ile Ala Pro Cys Tyr Gln Asp		
97 180 185 190		
99 tat gtg aaa aaa ttt gga gaa aat ttt gca tca tgt caa gct gga ata	624	
100 Tyr Val Lys Lys Phe Gly Glu Asn Phe Ala Ser Cys Gln Ala Gly Ile		
101 195 200 205		
103 tcc agt ttt tac aca aag gat tta att gtg atg ggg gcc cca gga tca	672	
104 Ser Ser Phe Tyr Thr Lys Asp Leu Ile Val Met Gly Ala Pro Gly Ser		
105 210 215 220		
107 tct tac tgg act ggc tct ctt gtc tac aat ata act aca aat aaa	720	
108 Ser Tyr Trp Thr Gly Ser Leu Phe Val Tyr Asn Ile Thr Thr Asn Lys		
109 225 230 235 240		
111 tac aag gct ttt tta gac aaa caa aat caa gta aaa ttt gga agt tat	768	
112 Tyr Lys Ala Phe Leu Asp Lys Gln Asn Gln Val Lys Phe Gly Ser Tyr		
113 245 250 255		
115 tta gga tat tca gtc gga gct ggt cat ttt cgg agc cag cat act acc	816	
116 Leu Gly Tyr Ser Val Gly Ala Gly His Phe Arg Ser Gln His Thr Thr		
117 260 265 270		
119 gaa gta gtc gga gga gct cct caa cat gag cag att ggt aag gca tat	864	
120 Glu Val Val Gly Gly Ala Pro Gln His Glu Gln Ile Gly Lys Ala Tyr		
121 275 280 285		
123 ata ttc agc att gat gaa aaa gaa cta aat atc tta cat gaa atg aaa	912	
124 Ile Phe Ser Ile Asp Glu Lys Glu Leu Asn Ile Leu His Glu Met Lys		
125 290 295 300		
127 ggt aaa aag ctt gga tcg tac ttt gga gct tct gtc tgt gct gtg gac	960	
128 Gly Lys Lys Leu Gly Ser Tyr Phe Gly Ala Ser Val Cys Ala Val Asp		
129 305 310 315 320		
131 ctc aat gca gat ggc ttc tca gat ctg ctc gtg gga gca ccc atg cag	1008	
132 Leu Asn Ala Asp Gly Phe Ser Asp Leu Leu Val Gly Ala Pro Met Gln		

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133	325	330	335	
135	agc acc atc aga gag gaa gga aga gtg ttt gtg tac atc aac tct ggc			1056
136	Ser Thr Ile Arg Glu Glu Gly Arg Val Phe Val Tyr Ile Asn Ser Gly			
137	340	345	350	
139	tcg gga gca gta atg aat gca atg gaa aca aac ctc gtt gga agt gac			1104
140	Ser Gly Ala Val Met Asn Ala Met Glu Thr Asn Leu Val Gly Ser Asp			
141	355	360	365	
143	aaa tat gct gca aga ttt ggg gaa tct ata gtt aat ctt ggc gac att			1152
144	Lys Tyr Ala Ala Arg Phe Gly Glu Ser Ile Val Asn Leu Gly Asp Ile			
145	370	375	380	
147	gac aat gat ggc ttt gaa gat gtt gct atc gga gct cca caa gaa gat			1200
148	Asp Asn Asp Gly Phe Glu Asp Val Ala Ile Gly Ala Pro Gln Glu Asp			
149	385	390	395	400
151	gac ttg caa ggt gct att tat att tac aat ggc cgt gca gat ggg atc			1248
152	Asp Leu Gln Gly Ala Ile Tyr Ile Tyr Asn Gly Arg Ala Asp Gly Ile			
153	405	410	415	
155	tcg tca acc ttc tca cag aga att gaa gga ctt cag atc agc aaa tcg			1296
156	Ser Ser Thr Phe Ser Gln Arg Ile Glu Gly Leu Gln Ile Ser Lys Ser			
157	420	425	430	
159	tta agt atg ttt gga cag tct ata tca gga caa att gat gca gat aat			1344
160	Leu Ser Met Phe Gly Gln Ser Ile Ser Gly Gln Ile Asp Ala Asp Asn			
161	435	440	445	
163	aat ggc tat gta gat gta gca gtt ggt gct ttt cgg tct gat tct gct			1392
164	Asn Gly Tyr Val Asp Val Ala Val Gly Ala Phe Arg Ser Asp Ser Ala			
165	450	455	460	
167	gtc ttg cta agg aca aga cct gta gta att gtt gac gct tct tta agc			1440
168	Val Leu Leu Arg Thr Arg Pro Val Val Ile Val Asp Ala Ser Leu Ser			
169	465	470	475	480
171	cac cct gag tca gta aat aga acg aaa ttt gac tgt gtt gaa aat gga			1488
172	His Pro Glu Ser Val Asn Arg Thr Lys Phe Asp Cys Val Glu Asn Gly			
173	485	490	495	
175	tgg cct tct gtg tgc ata gat cta aca ctt tgt ttc tca tat aag ggc			1536
176	Trp Pro Ser Val Cys Ile Asp Leu Thr Leu Cys Phe Ser Tyr Lys Gly			
177	500	505	510	
179	aag gaa gtt cca ggt tac att gtt ttg ttt tat aac atg agt ttg gat			1584
180	Lys Glu Val Pro Gly Tyr Ile Val Leu Phe Tyr Asn Met Ser Leu Asp			
181	515	520	525	
183	gtg aac aga aag gca gag tct cca cca aga ttc tat ttc tct tct aat			1632
184	Val Asn Arg Lys Ala Glu Ser Pro Pro Arg Phe Tyr Phe Ser Ser Asn			
185	530	535	540	
187	gga act tct gac gtg att aca gga agc ata cag gtg tcc agc aga gaa			1680
188	Gly Thr Ser Asp Val Ile Thr Gly Ser Ile Gln Val Ser Ser Arg Glu			
189	545	550	555	560
191	gct aac tgt aga aca cat caa gca ttt atg cgg aaa gat gtg cgg gac			1728
192	Ala Asn Cys Arg Thr His Gln Ala Phe Met Arg Lys Asp Val Arg Asp			
193	565	570	575	
195	atc ctc acc cca att cag att gaa gct gct tac cac ctt ggt cct cat			1776
196	Ile Leu Thr Pro Ile Gln Ile Glu Ala Ala Tyr His Leu Gly Pro His			
197	580	585	590	

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199 gtc atc agt aaa cga agt aca gag gaa ttc cca cca ctt cag cca att	1824
200 Val Ile Ser Lys Arg Ser Thr Glu Glu Phe Pro Pro Leu Gln Pro Ile	
201 595 600 605	
203 ctt cag cag aag aaa gaa aaa gac ata atg aaa aaa aca ata aac ttt	1872
204 Leu Gln Gln Lys Lys Glu Lys Asp Ile Met Lys Lys Thr Ile Asn Phe	
205 610 615 620	
207 gca agg ttt tgt gcc cat gaa aat tgt tct gct gat tta cag gtt tct	1920
208 Ala Arg Phe Cys Ala His Glu Asn Cys Ser Ala Asp Leu Gln Val Ser	
209 625 630 635 640	
211 gca aag att ggg ttt ttg aag ccc cat gaa aat aaa aca tat ctt gct	1968
212 Ala Lys Ile Gly Phe Leu Lys Pro His Glu Asn Lys Thr Tyr Leu Ala	
213 645 650 655	
215 gtt ggg agt atg aag aca ttg atg ttg aat gtg tcc ttg ttt aat gct	2016
216 Val Gly Ser Met Lys Thr Leu Met Leu Asn Val Ser Leu Phe Asn Ala	
217 660 665 670	
219 gga gat gat gca tat gaa acg act cta cat gtc aaa cta ccc gtg ggt	2064
220 Gly Asp Asp Ala Tyr Glu Thr Thr Leu His Val Lys Leu Pro Val Gly	
221 675 680 685	
223 ctt tat ttc att aag att tta gag ctg gaa gag aag caa ata aac tgt	2112
224 Leu Tyr Phe Ile Lys Ile Leu Glu Leu Glu Lys Gln Ile Asn Cys	
225 690 695 700	
227 gaa gtc aca gat aac tct ggc gtg gta caa ctt gac tgc agt att ggc	2160
228 Glu Val Thr Asp Asn Ser Gly Val Val Gln Leu Asp Cys Ser Ile Gly	
229 705 710 715 720	
231 tat ata tat gta gat cat ctc tca agg ata gat att agc ttt ctc ctg	2208
232 Tyr Ile Tyr Val Asp His Leu Ser Arg Ile Asp Ile Ser Phe Leu Leu	
233 725 730 735	
235 gat gtg agc tca ctc agc aga gcg gaa gag gac ctc agt atc aca gtg	2256
236 Asp Val Ser Ser Leu Ser Arg Ala Glu Glu Asp Leu Ser Ile Thr Val	
237 740 745 750	
239 cat gct acc tgt gaa aat gaa gag gaa atg gac aat cta aag cac agc	2304
240 His Ala Thr Cys Glu Asn Glu Glu Met Asp Asn Leu Lys His Ser	
241 755 760 765	
243 aga gtg act gta gca ata cct tta aaa tat gag gtt aag ctg act gtt	2352
244 Arg Val Thr Val Ala Ile Pro Leu Lys Tyr Glu Val Lys Leu Thr Val	
245 770 775 780	
247 cat ggg ttt gta aac cca act tca ttt gtg tat gga tca aat gat gaa	2400
248 His Gly Phe Val Asn Pro Thr Ser Phe Val Tyr Gly Ser Asn Asp Glu	
249 785 790 795 800	
251 aat gag cct gaa acg tgc atg gtg gag aaa atg aac tta act ttc cat	2448
252 Asn Glu Pro Glu Thr Cys Met Val Glu Lys Met Asn Leu Thr Phe His	
253 805 810 815	
255 gtt atc aac act ggc aat agt atg gct ccc aat gtt agt gtg gaa ata	2496
256 Val Ile Asn Thr Gly Asn Ser Met Ala Pro Asn Val Ser Val Glu Ile	
257 820 825 830	
259 atg gta cca aat tct ttt agc ccc caa act gat aag ctg ttc aac att	2544
260 Met Val Pro Asn Ser Phe Ser Pro Gln Thr Asp Lys Leu Phe Asn Ile	
261 835 840 845	
263 ttg gat gtc cag act act act gga gaa tgc cac ttt gaa aat tat caa	2592

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264	Leu	Asp	Val	Gln	Thr	Thr	Gly	Glu	Cys	His	Phe	Glu	Asn	Tyr	Gln				
265	850				855											860			
267	aga	gtg	tgt	gca	tta	gag	cag	caa	aag	agt	gca	atg	cag	acc	ttg	aaa	2640		
268	Arg	Val	Cys	Ala	Leu	Glu	Gln	Gln	Lys	Ser	Ala	Met	Gln	Thr	Leu	Lys			
269	865				870							875				880			
271	ggc	ata	gtc	cg	ttc	ttg	tcc	aag	act	gat	aag	agg	cta	ttg	tac	tgc	2688		
272	Gly	Ile	Val	Arg	Phe	Leu	Ser	Lys	Thr	Asp	Lys	Arg	Leu	Leu	Tyr	Cys			
273		885											890			895			
275	ata	aaa	gct	gat	cca	cat	tgt	tta	aat	ttc	ttg	tgt	aat	ttt	ggg	aaa	2736		
276	Ile	Lys	Ala	Asp	Pro	His	Cys	Leu	Asn	Phe	Leu	Cys	Asn	Phe	Gly	Lys			
277		900											905			910			
279	atg	gaa	agt	gga	aaa	gaa	gcc	agt	gtt	cat	atc	caa	ctg	gaa	ggc	cg	2784		
280	Met	Glu	Ser	Gly	Lys	Glu	Ala	Ser	Val	His	Ile	Gln	Leu	Glu	Gly	Arg			
281		915										920				925			
283	cca	tcc	att	tta	gaa	atg	gat	gag	act	tca	gca	ctc	aag	ttt	gaa	ata	2832		
284	Pro	Ser	Ile	Leu	Glu	Met	Asp	Glu	Thr	Ser	Ala	Leu	Lys	Phe	Glu	Ile			
285		930										935				940			
287	aga	gca	aca	ggt	ttt	cca	gag	cca	aat	cca	aga	gta	att	gaa	cta	aac	2880		
288	Arg	Ala	Thr	Gly	Phe	Pro	Glu	Pro	Asn	Pro	Arg	Val	Ile	Glu	Leu	Asn			
289		945										950				960			
291	aag	gat	gag	aat	gtt	g	cg	cat	gtt	cta	ctg	gaa	gga	cta	cat	cat	caa	2928	
292	Lys	Asp	Glu	Asn	Val	Ala	His	Val	Leu	Leu	Glu	Gly	Leu	His	His	Gln			
293			965									970				975			
295	aga	ccc	aaa	cgt	tat	ttc	acg	gat	ccc	gag	ctg	ctg	gga	ag	cagg	ctc	agc	2978	
296	Arg	Pro	Lys	Arg	Tyr	Phe	Thr	Asp	Pro	Glu									
297		980										985							
299	gtc	c	tc	tc	tc	tc	tc	tc	3038										
300	gtc	tc	tc	tc	tc	tc	tc	tc	tc	tc	tc	tc	tc	tc	tc	tc	tc	3098	
301	gg	ctt	ttt	ttt	ttt	ttt	ttt	ttt	3158										
302	caa	agg	gg	gg	gg	gg	gg	gg	3218										
303	tg	ac	cc	cc	cc	cc	cc	cc	3278										
304	ct	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	3333	
305	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	Glu Pro Lys Ser Cys Asp		
306																990			
308	aaa	act	cac	aca	tgc	cca	ccg	tgc	cca	gt	taa	g	cc	ag	cc	ag	cc	3380	
309	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro										
310		995										1000							
312	gc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	3440	
313	ag	cc	gg	gg	gg	gg	gg	gg	3494										
314																	His Leu Asn Ser Trp		
315																	1005		
317	gg	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	3542	
318	Gly	Asp	Arg	Gln	Ser	Ser	Ser	Ser	Pro	Gln	Asn	Pro	Arg	Thr	Pro	Ser			
319		1010										1015					1020		
321	tga	tct	ccc	gga	ccc	ctg	agg	tca	cat	g	cg	tgg	tgg	tgg	acg	tga	gcc	3590	
322	*	Ser	Pro	Gly	Pro	Leu	Arg	Ser	His	Ala	Trp	Trp	Trp	Trp	Trp	Trp	Trp	* Ala	
323		1025										1030					1035		
325	acg	aag	acc	ctg	agg	tca	agt	tca	act	ggt	acg	tgg	acg	g	cg	tgg	agg	3638	
326	Thr	Lys	Thr	Leu	Arg	Ser	Ser	Ser	Thr	Gly	Thr	Trp	Thr	Ala	Trp	Arg			

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L:38 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:41 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:44 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:47 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:50 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:384 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:387 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:390 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:393 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:396 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:852 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:855 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:19
L:858 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:19
L:861 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:19
L:864 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:19